

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/516,361A
Source: P4/10
Date Processed by STIC: 1/13/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/516,361A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 ☐ Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 ☐ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 ☒ Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

- 9 ☐ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 ☒ Invalid <213>
Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 ☐ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 ☐ Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 01/13/2006

PATENT APPLICATION: US/10/516,361A

TIME: 10:50:50

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\01132006\J516361A.raw

*see item 4 on
Errn summary sheet*

2 <110> APPLICANT: Islam Amirul
3 Hazra Papia
5 <120> TITLE OF INVENTION: An improved method of detection of target nucleic acid
sequence by
6 nucleic acid amplification
8 <130> FILE REFERENCE: 3875.033
10 <140> CURRENT APPLICATION NUMBER: US 10/516,361A
C--> 11 <141> CURRENT FILING DATE: 2004-11-30
13 <150> PRIOR APPLICATION NUMBER: PCT/IN 03/00204
W--> 14 <151> PRIOR FILING DATE: 2003.05.30 2003-05-30 ← *use this format for dates*
16 <150> PRIOR APPLICATION NUMBER: 487/MUM/2002 (IN)
W--> 17 <151> PRIOR FILING DATE: 2002.05.31 2002-05-31 ←
19 <160> NUMBER OF SEQ ID NOS: 31

ERRORED SEQUENCES

21 <210> SEQ ID NO: 1 *invalid response*
22 <211> LENGTH: 20 *(see item 10 on Errn summary sheet)*
23 <212> TYPE: DNA
E--> 24 <213> ORGANISM: Artificial / Unknown Sequence **Does Not Comply
Corrected Diskette Needed**
26 <220> FEATURE:
27 <221> NAME/KEY: primer_bind
28 <222> LOCATION:
29 <223> OTHER INFORMATION: Forward PCR primer for amplification of a target
30 sequence chosen arbitrarily and made from sequence
31 IDs 3 & 4.
33 <400> SEQUENCE: 1
34 acttaagtta gagcgtttgc 20
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 20
39 <212> TYPE: DNA
E--> 40 <213> ORGANISM: Artificial / Unknown Sequence *same error*
42 <220> FEATURE:
43 <221> NAME/KEY: primer_bind
44 <222> LOCATION:
45 <223> OTHER INFORMATION: Reverse PCR primer for amplification of a target
46 sequence chosen arbitrarily and made from sequence
47 IDs 3 & 4.
49 <400> SEQUENCE: 2
50 tggtagtatg tgatttagtc 20
53 <210> SEQ ID NO: 3
54 <211> LENGTH: 40
55 <212> TYPE: DNA

RAW SEQUENCE LISTING

DATE: 01/13/2006

PATENT APPLICATION: US/10/516,361A

TIME: 10:50:50

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\01132006\J516361A.raw

E--> 56 <213> ORGANISM: Artificial / Unknown Sequence

58 <220> FEATURE:

59 <221> NAME/KEY: misc_difference

60 <222> LOCATION:

61 <223> OTHER INFORMATION: Arbitrarily chosen sequence. Base 27 to 40 are
 62 complementary to basis 31 to 44 of sequence ID 4. *Bases*
 63 DNA polymerase extension of annealed Sequence IDs 3 *extension*
 64 & 4 results in the target sequence

66 <400> SEQUENCE: 3

67 tacacttaag ttagagcggt tgcgcccact acgacgggtg 40

71 <210> SEQ ID NO: 4

72 <211> LENGTH: 44

73 <212> TYPE: DNA

E--> 74 <213> ORGANISM: Artificial / Unknown Sequence

76 <220> FEATURE:

77 <221> NAME/KEY: misc_difference

78 <222> LOCATION:

79 <223> OTHER INFORMATION: Arbitrarily chosen sequence. Base 27 to 40 are
 80 complementary to basis 31 to 44 of sequence ID 4. *Bases*
 81 DNA polymerase extension of annealed Sequence IDs 3
 82 & 4 results in the target sequence

84 <400> SEQUENCE: 4

E--> 85 gtttttgtgg tagtatgtga tttagtcatt caaccgtcgt agtg 44 (see item 1 on
 86 44 Error Summary
 87 sheet)

89 <210> SEQ ID NO: 5

90 <211> LENGTH: 20

91 <212> TYPE: DNA

E--> 92 <213> ORGANISM: Artificial / Unknown Sequence

94 <220> FEATURE:

95 <221> NAME/KEY: primer_bind

96 <222> LOCATION:

97 <223> OTHER INFORMATION: Forward PCR primer for amplification of a target
 98 sequence chosen arbitrarily and made from sequence
 99 IDs 3 & 4. Base t at base position 18 from 5' end is having
 100 fluorophore FAM

102 <400> SEQUENCE: 5

103 acttaagtta gacggtttgc 20

see pp 3-5 for more errors

10/5/361A 3

<210> 30
<211> 20
<212> DNA
<213> E. Coli k-12

<220>
<221> Primer bind rpsT gene ? "+" is at 5' end
<222> Base g at 5' end is base 21303
<223> Reverse PCR primer. (Complementary)

<400> 30
ttaaaccggcg attgagtacc

20

10/8/36/A

4

<400> 31

agccttatga cgtgcagctt

20

delete this

Statement:

It is hereby declared that the sequence listing does not go beyond the content of the application as filed.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/516,361A

DATE: 01/13/2006
TIME: 10:50:51

FYI

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\01132006\J516361A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

(
Seq#:19; Line(s) 297
Seq#:20; Line(s) 311
Seq#:28; Line(s) 433

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/516,361A

DATE: 01/13/2006

TIME: 10:50:51

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\01132006\J516361A.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
 L:17 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
 L:24 M:251 E: Invalid Description for Numeric Identifier, <213> ORGANISM has both "Artificial" and "Unknown" for SEQ ID#:1
 L:40 M:251 E: Invalid Description for Numeric Identifier, <213> ORGANISM has both "Artificial" and "Unknown" for SEQ ID#:2
 L:56 M:251 E: Invalid Description for Numeric Identifier, <213> ORGANISM has both "Artificial" and "Unknown" for SEQ ID#:3
 L:74 M:251 E: Invalid Description for Numeric Identifier, <213> ORGANISM has both "Artificial" and "Unknown" for SEQ ID#:4
 L:85 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:44 SEQ:4
 L:92 M:251 E: Invalid Description for Numeric Identifier, <213> ORGANISM has both "Artificial" and "Unknown" for SEQ ID#:5
 L:112 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
 L:125 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
 L:141 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
 L:155 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
 L:169 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
 L:183 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
 L:197 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
 L:211 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
 L:225 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
 L:239 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
 L:253 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
 L:267 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
 L:281 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
 L:295 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
 L:309 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
 L:325 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
 L:341 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
 L:356 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
 L:371 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
 L:386 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
 L:401 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
 L:416 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
 L:431 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
 L:446 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
 L:461 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30
 L:475 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
 L:483 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:485 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
 L:485 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
 L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
 L:486 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5